

#2



OIEP

RAW SEQUENCE LISTING

DATE: 04/17/2002

PATENT APPLICATION: US/10/020,618

TIME: 11:53:16

Input Set : N:\Crf3\RULE60\10020618.raw

Output Set: N:\CRF3\04172002\J020618.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Bandman, Olga
6 Goli, Surya K.

8 (ii) TITLE OF INVENTION: A NOVEL H-REV107-LIKE
9 PROTEIN

11 (iii) NUMBER OF SEQUENCES: 4

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15 (B) STREET: 3174 Porter Drive
16 (C) CITY: Palo Alto
17 (D) STATE: CA
18 (E) COUNTRY: USA
19 (F) ZIP: 94304

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: DOS
25 (D) SOFTWARE: FastSEQ for Windows Version 2.0

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/020,618
C--> 29 (B) FILING DATE: 06-Dec-2001
30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 08/801,742
34 (B) FILING DATE:

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Billings, Lucy J.
38 (B) REGISTRATION NUMBER: 36,749
39 (C) REFERENCE/DOCKET NUMBER: PF-0200 US

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 415-855-0555
43 (B) TELEFAX: 415-845-4166

45 (2) INFORMATION FOR SEQ ID NO: 1:

47 (i) SEQUENCE CHARACTERISTICS:

48 (A) LENGTH: 164 amino acids
49 (B) TYPE: amino acid
50 (C) STRANDEDNESS: single
51 (D) TOPOLOGY: linear

54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

56 Met Ala Ser Pro His Gln Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
57 1 5 10 15
58 Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Gly Asp Gly Tyr

ENTERED

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```

59          20          25          30
60 Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
61          35          40          45
62 Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
63          50          55          60
64 Leu Glu Asp Val Val Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
65          65          70          75          80
66 Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
67          85          90          95
68 Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
69          100          105          110
70 Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
71          115          120          125
72 Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
73          130          135          140
W--> 74 Ile Leu Val Val Ala Gly Cys Ser Phe Xaa Ile Arg Arg Tyr Gln Lys
75          145          150          155          160
76 Lys Ala Thr Ala
79 (2) INFORMATION FOR SEQ ID NO: 2:
81   (i) SEQUENCE CHARACTERISTICS:
82       (A) LENGTH: 577 base pairs
83       (B) TYPE: nucleic acid
84       (C) STRANDEDNESS: single
85       (D) TOPOLOGY: linear
88   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
90 AAACAAGAGG AGCACCAGAC CTCCTCTTGG CTTGAGATG GCTTCGCCAC ACCAAGAGCC      60
91 CAAACCTGGA GACCTGATTG AGATTTTCCG CCTTGGCTAT GAGCACTGGG CCCTGTATAT      120
92 AGGAGATGGC TACGTGATCC ATCTGGCTCC TCCAAGTGAG TACCCCGGGG CTGGCTCCTC      180
93 CAGTGTCTTC TCAGTCCTGA GCAACAGTGC AGAGGTGAAA CGGGAGCGCC TGGAAGATGT      240
94 GGTGGGAGGC TGTGCTATC GGGTCAACAA CAGCTTGGAC CATGAGTACC AACCACGGCC      300
95 CGTGGAGGTG ATCATCAGTT CTGCGAAGGA GATGGTTGGT CAGAAGATGA AGTACAGTAT      360
96 TGTGAGCAGG AACTGTGAGC ACTTTGTCAC CCAGCTGAGA TATGGCAAGT CCCGCTGTAA      420
97 ACAGGTGGAA AAGGCCAAGG TTGAAGTCGG TGTGGCCACG GCGCTTGGAA TCCTGGTTGT      480
98 TGCTGGATGC TCTTTTNGA TTAGGAGATA CCAAAAAAAAA GCGACAGCCT GAAGCAGCCA      540
99 CAAAATCCTG TGTTAGAAGC AGCTGTGGGG GTCCCAA      577
101 (2) INFORMATION FOR SEQ ID NO: 3:
103   (i) SEQUENCE CHARACTERISTICS:
104       (A) LENGTH: 162 amino acids
105       (B) TYPE: amino acid
106       (C) STRANDEDNESS: single
107       (D) TOPOLOGY: linear
109   (vii) IMMEDIATE SOURCE:
110       (A) LIBRARY: GenBank
111       (B) CLONE: 1054752
113   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
115 Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
116   1          5          10          15
117 Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
118          20          25          30

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```

119 Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
120      35      40      45
121 Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
122      50      55      60
123 Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
124      65      70      75      80
125 Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
126      85      90      95
127 Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
128      100      105      110
129 Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
130      115      120      125
131 Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
132      130      135      140
133 Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
134      145      150      155      160
135 Lys Gln
138 (2) INFORMATION FOR SEQ ID NO: 4:
140 (i) SEQUENCE CHARACTERISTICS:
141 (A) LENGTH: 160 amino acids
142 (B) TYPE: amino acid
143 (C) STRANDEDNESS: single
144 (D) TOPOLOGY: linear
146 (vii) IMMEDIATE SOURCE:
147 (A) LIBRARY: GenBank
148 (B) CLONE: 1709969
150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
152 Met Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile Phe Arg
153 1      5      10      15
154 Pro Met Tyr Ser His Trp Ala Ile Tyr Val Gly Asp Gly Tyr Val Ile
155      20      25      30
156 His Leu Ala Pro Pro Ser Glu Ile Pro Gly Ala Gly Ala Ala Ser Ile
157      35      40      45
158 Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu Leu Arg
159      50      55      60
160 Asp Val Ala Gly Lys Asp Lys Tyr Gln Val Asn Asn Lys His Asp Lys
161      65      70      75      80
162 Glu Tyr Thr Pro Leu Pro Leu Asn Lys Ile Ile Gln Arg Ala Glu Glu
163      85      90      95
164 Leu Val Gly Gln Glu Val Leu Tyr Arg Leu Thr Ser Glu Asn Cys Glu
165      100      105      110
166 His Phe Val Asn Glu Leu Arg Tyr Gly Val Pro Arg Ser Asp Gln Val
167      115      120      125
168 Arg Asp Thr Val Lys Val Ala Thr Val Thr Gly Val Gly Leu Ala Ala
169      130      135      140
170 Leu Gly Leu Ile Gly Val Met Leu Ser Arg Asn Lys Lys Gln Lys Gln
171      145      150      155      160

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1